

CLAIMS

What is claimed is:

1. A method of reducing storage requirements for identifying a sequence of elements in a compound, comprising:

receiving a set of monoisotopic masses designed to address entries from two or more mass spectroscopy data sets according to a fitness function;

analyzing the fitness function configured to facilitate identification of a sequence of elements in the compound;

determining a minimum address range for addressing entries in each of the two or more mass spectroscopy data sets according to sequence of elements and fitness function analysis; and

reducing the size of at least one of the two or more mass spectroscopy data sets to selected mass data values according to the minimum address range.

2. The method of claim 1 further comprising,

using an offset from one or more monoisotopic mass tables in combination with additional logic to address the selected mass data values in the at least one of the two or more reduced mass spectroscopy data sets.

3. The method of claim 2 wherein the additional logic includes a concatenation of the offset values from the one or more monoisotopic mass tables to address the selected mass data values.

4. The method of claim 1 wherein the monoisotopic masses are designed to address entries from two or more mass spectroscopy data sets in parallel.

5. The method of claim 1 wherein the sequence of elements in the compound corresponds to a sequence of amino acids in a protein.

6. The method of claim 1 wherein the analysis of the fitness function includes identifying entries in at least one of the two or more mass spectroscopy data sets that inherently cannot be addressed due to characteristics of the fitness function.

7. The method of claim 6 wherein the characteristics of the fitness function allows for addressing only a smaller subset of the addresses in one of the two or more mass spectroscopy data sets.

8. The method of claim 1 wherein the selected mass data values are associated with addresses within the minimum address range.

9. A method of identifying a sequence of elements in a compound with reduced storage requirements, comprising:

receiving a set of monoisotopic mass lookup tables for accessing two or more mass spectroscopy data sets in parallel according to a fitness function;

identifying a first portion of addresses determined directly from offset values corresponding to a monoisotopic mass lookup table from the set of monoisotopic mass lookup tables;

accessing a selected number of mass spectroscopy data set values for the compound using additional logic and the offset values directly; and

evaluating the fitness function to determine elements in the compound based upon mass spectroscopy data set values accessed directly from the offset values corresponding to the monoisotopic mass lookup table.

10. The method of claim 9 further comprising:
identifying a combination of elements in a compound according to the fitness function evaluation.

11. The method of claim 9 wherein the compound is a protein and the

elements correspond to one or more amino acids.

12. The method of claim 9 further comprising:

identifying a second portion of addresses determined indirectly from a mass value entered at an offset in a monoisotopic lookup table; and

accessing mass spectroscopy data set values based on a mass value at the offset in the one or more monoisotopic lookup tables.

13. The method of claim 12 wherein evaluating the fitness function is further based upon mass spectroscopy data set values accessed indirectly from the mass value at the offset in the one or more monoisotopic lookup table.

14. A computer program product for reducing storage requirements when identifying a sequence of elements in a compound, tangibly stored on a computer-readable medium, comprising instructions operable to cause a programmable processor to:

receive a set of monoisotopic masses designed to address entries from two or more mass spectroscopy data sets according to a fitness function;

analyze the fitness function configured to facilitate identification of a sequence of elements in the compound;

determine a minimum address range for addressing entries in each of the two or more mass spectroscopy data sets according to sequence of elements and fitness function analysis; and

reduce the size of at least one of the two or more mass spectroscopy data sets to selected mass data values according to the minimum address range.

15. The computer program product of claim 14 further comprising instructions operable to cause a programmable processor to,

use an offset from one or more monoisotopic mass tables in combination with additional logic to address the selected mass data values in the at least one of the two or more reduced mass spectroscopy data sets.

16. The computer program product of claim 15 wherein the additional logic includes a concatenation of the offset values from the one or more monoisotopic mass tables to address the selected mass data values.

17. The computer program product of claim 14 wherein the monoisotopic masses are designed to address entries from two or more mass spectroscopy data sets in parallel.

18. The computer program product of claim 14 wherein the sequence of elements in the compound corresponds to a sequence of amino acids in a protein.

19. The computer program product of claim 14 wherein the analysis of the fitness function includes identifying entries in at least one of the two or more mass spectroscopy data sets that inherently cannot be addressed due to characteristics of the fitness function.

20. The computer program product of claim 19 wherein the characteristics of the fitness function allows for addressing only a smaller subset of the addresses in one of the two or more mass spectroscopy data sets.

21. The computer program product of claim 14 wherein the selected mass spectroscopy data set values are associated with addresses within the minimum address range.

22. A computer program product for identifying a sequence of elements in a compound with reduced storage requirements, tangibly stored on a computer-readable medium, comprising instructions operable to cause a programmable processor to:

receive a set of monoisotopic mass lookup tables for accessing two or more mass spectroscopy data sets in parallel according to a fitness function;

identify a first portion of addresses determined directly from offset values corresponding to a monoisotopic mass lookup table from the set of monoisotopic mass lookup tables;

access a selected number of mass spectroscopy data set values for the compound using additional logic and the offset values directly; and

evaluate the fitness function to determine elements in the compound based upon mass spectroscopy data set values accessed directly from the offset values corresponding to the monoisotopic mass lookup table.

23. The computer program product of claim 22 further comprising instructions operable to cause a programmable processor to:

identify a combination of elements in a compound according to the fitness function evaluation.

24. The computer program product of claim 22 wherein the compound is a protein and the elements correspond to one or more amino acids.

25. The computer program product of claim 22 further comprising instructions operable to cause a programmable processor to:

identify a second portion of addresses determined indirectly from a mass value entered at an offset in a monoisotopic lookup table; and

access mass spectroscopy data set values based on a mass value at the offset in the one or more monoisotopic lookup tables.

26. The computer program product of claim 22 wherein evaluating the fitness function is further based upon mass spectroscopy data set values accessed indirectly from

the mass value at the offset in the one or more monoisotopic mass lookup tables.

27. An apparatus for reducing storage requirements for identifying a sequence of elements in a compound, comprising:

means for receiving a set of monoisotopic masses designed to address entries from two or more mass spectroscopy data sets according to a fitness function;

means for analyzing the fitness function configured to facilitate identification of a sequence of elements in the compound;

means for determining a minimum address range for addressing entries in each of the two or more mass spectroscopy data sets according to sequence of elements and fitness function analysis; and

means for reducing the size of at least one of the two or more mass spectroscopy data sets to selected mass data values according to the minimum address range.

28. The apparatus of claim 27 further comprising,

means for using an offset from one or more monoisotopic mass tables in combination with additional logic to address the selected mass data values in the at least one of the two or more reduced mass spectroscopy data sets.

29. An apparatus for identifying a sequence of elements in a compound with reduced storage requirements, comprising:

means for receiving a set of monoisotopic mass lookup tables for accessing two or more mass spectroscopy data sets in parallel according to a fitness function;

means for identifying a first portion of addresses determined directly from offset values corresponding to a monoisotopic mass lookup table from the set of monoisotopic mass lookup tables;

means for accessing a selected number of mass spectroscopy data set values for

the compound using additional logic and the offset values directly; and

means for evaluating the fitness function to determine elements in the compound based upon mass spectroscopy data set values accessed directly from the offset values corresponding to the monoisotopic mass lookup table.

30. The apparatus of claim 29 further comprising:

means for identifying a combination of elements in a compound according to the fitness function evaluation.

31. An apparatus for reducing storage requirements identifying a sequence of elements in a compound, comprising:

a processor;

a memory containing instructions when executed on the processor cause the processor to receive a set of monoisotopic mass tables designed to address entries from two or more mass spectroscopy data sets according to a fitness function, analyzing the fitness function configured to facilitate identification of a sequence of elements in the compound, determining a minimum address range for addressing entries in each of the two or more mass spectroscopy data sets according to sequence of elements and fitness function analysis and reducing the size of at least one of the two or more mass spectroscopy data sets to selected mass data values according to the minimum address range.

32. An apparatus for identifying a sequence of elements in a compound with reduced storage requirements, comprising:

a processor;

a memory containing instructions when executed on the processor cause the processor to receive a set of monoisotopic mass lookup tables for accessing two or more

mass spectroscopy data sets in parallel according to a fitness function, identify a first portion of addresses determined directly from offset values corresponding to a monoisotopic mass lookup table from the set of monoisotopic mass lookup tables, access a selected number of mass spectroscopy data set values for the compound using additional logic and the offset values directly and evaluate the fitness function to determine elements in the compound based upon mass spectroscopy data set values accessed directly from the offset values corresponding to the monoisotopic mass lookup table.